



IFW16

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/890,813A

DATE: 08/26/2004  
TIME: 11:31:08

Input Set : A:\BB1430 US PCT Corrected Sequence Listing.txt  
Output Set: N:\CRF4\08262004\I890813A.raw

3 <110> APPLICANT: E.I. du Pont de Nemours and Company  
5 <120> TITLE OF INVENTION: Aspartate Kinase  
7 <130> FILE REFERENCE: BB1430 PCT  
9 <140> CURRENT APPLICATION NUMBER: 09/890813A  
10 <141> CURRENT FILING DATE: 2001-08-02  
12 <150> PRIOR APPLICATION NUMBER: PCT/US00/34396  
13 <151> PRIOR FILING DATE: 2000-12-19  
15 <150> PRIOR APPLICATION NUMBER: 60/172944  
16 <151> PRIOR FILING DATE: 1999-12-21  
18 <160> NUMBER OF SEQ ID NOS: 28  
20 <170> SOFTWARE: PatentIn version 3.2  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 565  
24 <212> TYPE: DNA  
25 <213> ORGANISM: Zea mays  
27 <220> FEATURE:  
28 <221> NAME/KEY: unsure  
29 <222> LOCATION: (127)  
30 <223> OTHER INFORMATION: n=a,c,g or t  
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34 aatttcactt atcggaaatg tggagcaatc gtctctata ctagaaaaga cgggacgtgt 120  
W--> 35 gctgagngaa agtggggtta atgttcagat gatctcgaa ggagcgtcaa aggttaacat 180  
36 gtcgtgtata gtccatgata gcgatgcaaa ggcactcgta gaagcccttc atcaggcggtt 240  
37 ctttgaagac gatgtcctat cacaagtcga agcggagaac ctactcgtgg gctgatcaac 300  
38 gtaggctttg ctgggtccag gcgtgttatac tgttatagat tcccaactcgc ctccatgaac 360  
39 ggcattggca ttggatcatt gatcatgtt tgctgaaac aagtatgtct tccaggttct 420  
40 cagccaatga ctgcaaaact gtgttctgt tttagaactg tttgcagaca ccagtgagct 480  
41 gcgagcaccg attgtcaaca agatggcaag cctgtgatat aattccaact gtctctaatac 540  
42 aatatataataaacatata tcaat 565  
45 <210> SEQ ID NO: 2  
46 <211> LENGTH: 97  
47 <212> TYPE: PRT  
48 <213> ORGANISM: Zea mays  
50 <220> FEATURE:  
51 <221> NAME/KEY: unsure  
52 <222> LOCATION: (42)  
53 <223> OTHER INFORMATION: Xaa=any amino acid  
55 <400> SEQUENCE: 2  
56 His Glu Val Glu Glu Leu Glu Lys Ile Ala Ile Val Arg Leu Leu Gln  
57 1 5 10 15  
59 Gln Arg Ala Ile Ile Ser Leu Ile Gly Asn Val Glu Gln Ser Ser Leu  
60 20 25 30



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--> 62 Ile Leu Glu Lys Thr Gly Arg Val Leu Xaa Glu Ser Gly Val Asn Val  
 63 35 40 45  
 65 Gln Met Ile Ser Gln Gly Ala Ser Lys Val Asn Met Ser Leu Ile Val  
 66 50 55 60  
 68 His Asp Ser Asp Ala Lys Ala Leu Val Glu Ala Leu His Gln Ala Phe  
 69 65 70 75 80  
 71 Phe Glu Asp Asp Val Leu Ser Gln Val Glu Ala Glu Asn Leu Leu Val  
 72 85 90 95  
 74 Gly  
 76 <210> SEQ ID NO: 3  
 77 <211> LENGTH: 513  
 78 <212> TYPE: DNA  
 79 <213> ORGANISM: Zea mays  
 81 <220> FEATURE:  
 82 <221> NAME/KEY: unsure  
 83 <222> LOCATION: (474)  
 84 <223> OTHER INFORMATION: n=a,c,g or t  
 86 <400> SEQUENCE: 3  
 87 acagagcagg aggactcaga aatggcaatc ccagtgcgtat cggctgcccgc gccccggccgc 60  
 88 ctcgttccgt cgataacctcc ggcgagctct ggacatgttc gaggactggc gtgttcgggt 120  
 89 acccgaaaccg ggcctcgcgg tgcaagaggg ttgtcaatgg tggtcgcccga ctccaccagc 180  
 90 cgtcggggcca agcaagcggg cggcggggac ggcgtccttgc gggcgccctgt tctcggaggg 240  
 91 ctcgggatgg agggattggg gatatcagtc agcgtggtga tgaagttcgg ggggtcctcg 300  
 92 gtgtcgtcgg ccgcgaggat ggctgaggtg gccggcctca tcctgacgtt ccccgaggag 360  
 93 cgcggcgtcg tcgttcttc tgccatggg aaaaccacca acaacccttct ccttgctggg 420  
 --> 94 agaaaaggca ataagggtgtg gagttatcat gtttctgaa atccgaagaa tggnatatgg 480  
 95 tcaaaaagcc taaaatatac aagtatccca act 513  
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 98 <211> LENGTH: 152  
 99 <212> TYPE: PRT  
 100 <213> ORGANISM: Zea mays  
 102 <400> SEQUENCE: 4  
 103 Thr Glu Gln Glu Asp Ser Glu Met Ala Ile Pro Val Arg Ser Ala Ala  
 104 1 5 10 15  
 106 Ala Pro Arg Arg Leu Val Pro Ser Ile Pro Pro Ala Ser Ser Gly His  
 107 20 25 30  
 109 Val Arg Gly Leu Ala Cys Phe Gly Thr Arg Thr Gly Pro Arg Gly Ala  
 110 35 40 45  
 112 Arg Gly Leu Ser Met Val Val Ala Asp Ser Thr Ser Arg Arg Ala Lys  
 113 50 55 60  
 115 Gln Ala Asp Gly Gly Asp Gly Val Leu Gly Ala Pro Val Leu Gly Gly  
 116 65 70 75 80  
 118 Leu Gly Met Glu Gly Leu Gly Asp Gln Leu Ser Val Val Met Lys Phe  
 119 85 90 95  
 121 Gly Gly Ser Ser Val Ser Ser Ala Ala Arg Met Ala Glu Val Ala Gly  
 122 100 105 110  
 124 Leu Ile Leu Thr Phe Pro Glu Glu Arg Pro Val Val Val Leu Ser Ala  
 125 115 120 125  
 127 Met Gly Lys Thr Thr Asn Asn Leu Leu Ala Gly Arg Lys Gly Asn

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128	130	135	140	
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131	145	150		
133	<210> SEQ ID NO: 5			
134	<211> LENGTH: 1985			
135	<212> TYPE: DNA			
136	<213> ORGANISM: Zea mays			
138	<220> FEATURE:			
139	<221> NAME/KEY: unsure			
140	<222> LOCATION: (532)			
141	<223> OTHER INFORMATION: n=a,c,g or t			
143	<220> FEATURE:			
144	<221> NAME/KEY: unsure			
145	<222> LOCATION: (1180)			
146	<223> OTHER INFORMATION: n=a,c,g or t			
148	<400> SEQUENCE: 5			
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150	ccgcgcctc gttccgtcga tacctccggc gagctctggc catgttcgag gactggcggt	120		
151	cttcggtaacc cgaaccgggc ctcgcgggtgc aagagggttg tcaatgggtgg tcgcccactc	180		
152	caccagccgt cgggccaaggc aaggccgacgg cggggacggc gtccttgggg cgcctgttct	240		
153	cggaggggctc gggatggagg gattggggga tcagctcagc gtggtgatga agttcggggg	300		
154	gtcctcggtg tgcgtggccg cgaggatggc tgaggtggcc ggctctatcc tgacgttccc	360		
155	cgaggagcgc cccgtcgctcg ttctctctgc catggggaaa accaccaaca acttctccct	420		
156	tgctggagag aaggcagtag ggtgtggagt tatccatgtt tctgaaatcg aagagtggaa	480		
W--> 157	tatggtcaaa agcctacata tcaagacgggt ggatgaactt ggacttccaa gnatctgtaa	540		
158	tacaagcctt tatgaacttgg agcaactatt gaaaggatgc gctatgtatga aagagctgac	600		
159	gccttaggacc agtgaactacc ttgtttcatt tggagaatgc atgtccacca ggattttttc	660		
160	tgcttatttg aacaaaattt cgtcaaggc acggcagttt gacgcattt atattggttt	720		
161	cattacaact gatgaatttt gtaatgcggta tatcttagaa gcaacctatc ctgctgtgc	780		
162	gaagagactt catggggact ggatacagga tccagcgata cctgttggta ctgggttccct	840		
163	tggaaaggcc tggaaatctg gtgcgtgtaac tacttttaggc cgaggtggta gtgacttgc	900		
164	tgctacaacc attggtaaaag ccttggact gagagaatt caggtatggaa aagatgttgc	960		
165	tggtgtactt acttgcgtatc caaatatcta cccacatgca aagactgttc cataacttaac	1020		
166	atttgaagag gccacagaac ttgcattttt tggtgctcag gtttgcatc cacaatcgat	1080		
167	gagacctgct agagaagggtt atattccagt tagggtaaag aattcataca accctaaagc	1140		
W--> 168	tccaggcacc cttattacca gacaaagaga catggataan ggtctgggttg tactaactag	1200		
169	catagtgctc aagtccaaatg tcactatgtt ggacattgtg agcactcgaa tgcttggtca	1260		
170	gtatggttt ctggcaagggt tatcaggtat ttgcataattt gaagatctat gtatatctgt	1320		
171	ggattgtgtt gtcaccatgtt aagttatgtt ttctgtgtca ctgtatccat caaagatctg	1380		
172	gagtagggaa ctgatacagc aggcaagtga acttgaccat gtatgttgc agcttgagaa	1440		
173	aatagcaatt gttcgctac ttccggcaggag ggccgataatt tcacttatcg gaaatgttgc	1500		
174	gcaatcgctc ctgataacttag aaaagacggg acgtgtgtc aggaaaaatgtt ggggttaatgt	1560		
175	tcagatgtatc tcgcaaggag cgtccaaagggt taacatgtcg ctgtatgtcc atgtatgcga	1620		
176	tgcggca ctcgttgcgtt cccttcatca ggcgttctt gaagacgtatc tccttatcaca	1680		
177	agtcaaggc gagaacctac tcgtgggtgtt atcaacgtatc gctttgttgc gtccaggcggt	1740		
178	gttatctgtt atagattccc actcgccctcc atgaacgcgt tggcattgg atcattgtatc	1800		
179	atgttttgct taaaacaatgtt atgtttccat ggttctcgatc caatgtatgc aaaactgtgt	1860		
180	ttctgttttta gaactgtttt cagacaccatc tgagctgcgt gcaccgattt tcaacaatgtt	1920		
181	ggcaaggctg tgcataattt ccaactgtatc ctaatcaata tatataataa acattatcaa	1980		

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182 tatct 1985  
 184 <210> SEQ ID NO: 6  
 185 <211> LENGTH: 560  
 186 <212> TYPE: PRT  
 187 <213> ORGANISM: Zea mays  
 189 <220> FEATURE:  
 190 <221> NAME/KEY: UNSURE  
 191 <222> LOCATION: (168)  
 192 <223> OTHER INFORMATION: Xaa=any amino acid  
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 195 <221> NAME/KEY: UNSURE  
 196 <222> LOCATION: (384)  
 197 <223> OTHER INFORMATION: Xaa=any amino acid  
 199 <400> SEQUENCE: 6  
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 201 1 5 10 15  
 203 Ser Ile Pro Pro Ala Ser Ser Gly His Val Arg Gly Leu Ala Cys Phe  
 204 20 25 30  
 206 Gly Thr Arg Thr Gly Pro Arg Gly Ala Arg Gly Leu Ser Met Val Val  
 207 35 40 45  
 209 Ala Asp Ser Thr Ser Arg Arg Ala Lys Gln Ala Asp Gly Gly Asp Gly  
 210 50 55 60  
 212 Val Leu Gly Ala Pro Val Leu Gly Gly Leu Gly Met Glu Gly Leu Gly  
 213 65 70 75 80  
 215 Asp Gln Leu Ser Val Val Met Lys Phe Gly Gly Ser Ser Val Ser Ser  
 216 85 90 95  
 218 Ala Ala Arg Met Ala Glu Val Ala Gly Leu Ile Leu Thr Phe Pro Glu  
 219 100 105 110  
 221 Glu Arg Pro Val Val Val Leu Ser Ala Met Gly Lys Thr Thr Asn Asn  
 222 115 120 125  
 224 Leu Leu Leu Ala Gly Glu Lys Ala Val Gly Cys Gly Val Ile His Val  
 225 130 135 140  
 227 Ser Glu Ile Glu Glu Trp Asn Met Val Lys Ser Leu His Ile Lys Thr  
 228 145 150 155 160  
 W--> 230 Val Asp Glu Leu Gly Leu Pro Xaa Ile Cys Asn Thr Ser Leu Tyr Glu  
 231 165 170 175  
 233 Leu Glu Gln Leu Leu Lys Gly Ile Ala Met Met Lys Glu Leu Thr Pro  
 234 180 185 190  
 236 Arg Thr Ser Asp Tyr Leu Val Ser Phe Gly Glu Cys Met Ser Thr Arg  
 237 195 200 205  
 239 Ile Phe Ser Ala Tyr Leu Asn Lys Ile Arg Val Lys Ala Arg Gln Tyr  
 240 210 215 220  
 242 Asp Ala Phe Asp Ile Gly Phe Ile Thr Thr Asp Glu Phe Gly Asn Ala  
 243 225 230 235 240  
 245 Asp Ile Leu Glu Ala Thr Tyr Pro Ala Val Ala Lys Arg Leu His Gly  
 246 245 250 255  
 248 Asp Trp Ile Gln Asp Pro Ala Ile Pro Val Val Thr Gly Phe Leu Gly  
 249 260 265 270  
 251 Lys Gly Trp Lys Ser Gly Ala Val Thr Thr Leu Gly Arg Gly Ser

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Input Set : A:\BB1430 US PCT Corrected Sequence Listing.txt  
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252	275	280	285													
254	Asp	Leu	Thr	Ala	Thr	Thr	Ile	Gly	Lys	Ala	Leu	Gly	Leu	Arg	Glu	Ile
255	290	295	300													
257	Gln	Val	Trp	Lys	Asp	Val	Asp	Gly	Val	Leu	Thr	Cys	Asp	Pro	Asn	Ile
258	305	310	315	320												
260	Tyr	Pro	His	Ala	Lys	Thr	Val	Pro	Tyr	Leu	Thr	Phe	Glu	Glu	Ala	Thr
261	325	330	335													
263	Glu	Leu	Ala	Tyr	Phe	Gly	Ala	Gln	Val	Leu	His	Pro	Gln	Ser	Met	Arg
264	340	345	350													
266	Pro	Ala	Arg	Glu	Gly	Asp	Ile	Pro	Val	Arg	Val	Lys	Asn	Ser	Tyr	Asn
267	355	360	365													
-> 269 Pro Lys Ala Pro Gly Thr Leu Ile Thr Arg Gln Arg Asp Met Asp Xaa																
270	370	375	380													
272	Gly	Leu	Val	Val	Leu	Thr	Ser	Ile	Val	Leu	Lys	Ser	Asn	Val	Thr	Met
273	385	390	395	400												
275	Leu	Asp	Ile	Val	Ser	Thr	Arg	Met	Leu	Gly	Gln	Tyr	Gly	Phe	Leu	Ala
276	405	410	415													
278	Arg	Val	Ser	Gly	Ile	Cys	Tyr	Ile	Glu	Asp	Leu	Cys	Ile	Ser	Val	Asp
279	420	425	430													
281	Cys	Val	Ala	Thr	Ser	Glu	Val	Ser	Val	Ser	Val	Ser	Leu	Asp	Pro	Ser
282	435	440	445													
284	Lys	Ile	Trp	Ser	Arg	Glu	Leu	Ile	Gln	Gln	Ala	Ser	Glu	Leu	Asp	His
285	450	455	460													
287	Val	Val	Glu	Glu	Leu	Glu	Lys	Ile	Ala	Ile	Val	Arg	Leu	Leu	Gln	Gln
288	465	470	475	480												
290	Arg	Ala	Ile	Ile	Ser	Leu	Ile	Gly	Asn	Val	Glu	Gln	Ser	Ser	Leu	Ile
291	485	490	495													
293	Leu	Glu	Lys	Thr	Gly	Arg	Val	Leu	Arg	Lys	Ser	Gly	Val	Asn	Val	Gln
294	500	505	510													
296	Met	Ile	Ser	Gln	Gly	Ala	Ser	Lys	Val	Asn	Met	Ser	Leu	Ile	Val	His
297	515	520	525													
299	Asp	Ser	Asp	Ala	Lys	Ala	Leu	Val	Glu	Ala	Leu	His	Gln	Ala	Phe	Phe
300	530	535	540													
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303	545	550	555	560												
305	<210>	SEQ ID NO:	7													
306	<211>	LENGTH:	1953													
307	<212>	TYPE:	DNA													
308	<213>	ORGANISM:	Zea mays													
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312	gttccgtcga	tacccctccgc	gagctctgg	catgttcgag	gactggcg	cttcgggtacc	120									
313	cgaaccgggc	ctcgccgtgc	aagagggttg	tcaatgg	tcgcccactc	caccagccgt	180									
314	cggggccaagc	aagcggacgg	cggggacggc	gtccttgggg	cgcctgttct	cgaggggctc	240									
315	gggatggagg	gatggggg	tcagctcagc	gtggatgat	agttcgggg	gtcctcggt	300									
316	tgcgtcgccg	cgaggatggc	tgaggtggcc	ggcctcatcc	tgacgttccc	cgaggagcgc	360									
317	cccggtcg	ttctctctgc	catggggaaa	accaccaaca	accttctct	tgcgtggag	420									
318	aaggcagtag	ggtgtggagt	tatccatgtt	tctgaaatcg	aagagtggaa	tatggtcaaa	480									
319	agcctacata	tcaagacggt	ggatgaactt	ggacttccaa	gatctgtta	acaagacatg	540									

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 127  
Seq#:2; Xaa Pos. 42  
Seq#:3; N Pos. 474  
Seq#:5; N Pos. 532,1180  
Seq#:6; Xaa Pos. 168,384  
Seq#:9; N Pos. 366,394,406,414,425,431,455  
Seq#:13; N Pos. 289,329,393,435,551,582,583,616,626,632,637,640  
Seq#:14; Xaa Pos. 110,131,145

## VERIFICATION SUMMARY

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Input Set : A:\BB1430 US PCT Corrected Sequence Listing.txt  
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L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:120  
L:62 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:32  
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:420  
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:480  
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1140  
L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:160  
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:368  
L:503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:360  
L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:420  
L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:240  
L:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:300  
L:684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:360  
L:685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:420  
L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:540  
L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:600  
L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:96  
L:735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:128  
L:738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:144